WE CLAIM:

1. An isolated nucleic acid comprising at least 12 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1; complementary sequence of SEQ ID NO 1, SEQ ID NO: 2, complementary sequence of SEQ ID NO 2; SEQ ID NO: 3; complementary sequence of SEQ ID NO. 3; SEQ ID NO: 4; complementary sequence of SEQ ID NO: 4; SEQ ID NO: 5; complementary sequence of SEQ ID NO: 5; SEQ ID NO: 6; complementary sequence of SEQ ID NO. 6; SEQ ID NO: 7; complementary sequence of SEQ ID NO 7; SEQ ID NO: 8; complementary sequence of SEQ ID NO. 8; SEQ ID NO: 9; complementary sequence of SEQ ID NO: 9; SEQ ID NO: 10; complementary sequence of SEQ ID NO: 10; SEQ ID NO: 11; complementary sequence of SEQ ID NO: 11; SEQ ID NO: 12; complementary sequence of SEQ ID NO: 12; SEQ ID NO: 13; complementary sequence of SEQ ID NO: 13; SEQ ID NO: 14; complementary sequence of SEQ ID NO: 14; SEQ ID NO: 15; complementary sequence of SEQ ID NO: 15; SEQ ID NO: 16; complementary sequence of SEQ ID NO: 16;SEQ ID NO: 17; complementary sequence of SEQ ID NO: 17; SEQ ID NO: 18; complementary sequence of SEQ ID NO: 18; SEQ ID NO: 19; complementary sequence of SEQ ID NO: 19; SEQ ID NO: 20; complementary sequence of SEQ ID NO: 20; SEQ ID NO: 21; complementary sequence of SEQ ID NO: 21; SEQ ID NO: 22; complementary sequence of SEQ ID NO: 22; SEQ ID NO: 23; complementary sequence of SEQ ID NO: 23; SEQ ID NO: 24; complementary sequence of SEQ ID NO: 24; SEQ ID NO: 25; complementary sequence of SEQ ID NO: 25; SEQ ID NO: 26; complementary sequence of SEQ ID NO: 26; SEQ ID NO: 27; complementary sequence of SEQ ID NO: 27; SEQ ID NO: 28; and complementary sequence of SEQ ID NO: 28.

2. The isolated nucleic acid of claim 1, wherein the nucleic acid comprises at least 15 consecutive nucleotides of the nucleotide sequence.

3. The isolated nucleic acid of claim 1, wherein the nucleic acid comprises at least 18 consecutive nucleotides of the nucleotide sequence.

4. The isolated nucleic acid of claim 1 immobilized on a solid surface.

5. The isolated nucleic acid of claim 1, wherein the nucleic acid is capable of detecting *Cannabis sativa* L.

6. The isolated nucleic acid of claim 1, wherein the isolated nucleic acid is capable of being used in a multiplex cocktail for amplification of a STR from *Cannabis sativa* L.

7. A pair of forward and reverse primers for amplification of a STR located in DNA isolated from *Cannabis sativa* L., said pair being selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 2; SEQ ID NO: 3 and SEQ ID NO: 4; SEQ ID NO: 5 and SEQ ID NO: 6; SEQ ID NO: 7 and SEQ ID NO: 8; SEQ ID NO: 9 and SEQ ID NO: 10; SEQ ID NO: 11 and SEQ ID NO: 12; SEQ ID NO: 13 and SEQ ID NO: 14; SEQ ID NO: 15 and SEQ ID NO: 16; and SEQ ID NO: 17 and SEQ ID NO: 18; SEQ ID NO: 19 and SEQ ID NO: 20; SEQ ID NO: 21 and SEQ ID NO: 22; SEQ ID NO: 23 and SEQ ID NO: 24; SEQ ID NO: 25 and SEQ ID NO: 26; and SEQ ID NO: 27 and SEQ ID NO: 28.

8. The pair of forward and reverse primers of claims 7, wherein a member of said pair comprises an observable marker.

9. The pair of forward and reverse primers of claim 8, wherein said marker is a fluorescent label.

10. The pair of forward and reverse primers of claim 8, wherein said marker is a radioactive group.

11. The pair of forward and reverse primers of claim 7 as PCR primers in the detection of a *Cannabis sativa* L. species.

12. The pair of forward and reverse primers of claim 7, wherein said pair is capable of being used in a multiplex cocktail for amplification of STR from *Cannabis sativa* L.

13. A method for detecting a *Cannabis sativa* L. species in a sample comprising the steps of:

i. obtaining DNA from the sample,

ii. amplifying a STR marker loci in said DNA with a multiplex cocktail of claim 7 to form amplification products of various sizes and labels; and

iii. separating amplification products by size and primer label;

iv. scoring the results of said separation; and

v. comparing said scored results to analysis of DNA from a known species.

14. A method of linking a marijuana sample to a plant source comprising the steps of:

i. determining the identity of DNA in said sample by the method of claim 13;

ii. determining the identity of DNA in a sample from a plant by the method of claim 13; and

iii. comparing the identities of both samples to determine similarities.

15. A kit for use in the detection of a *Cannabis sativa* L. species by multiplex cocktail comprising a primer pair of claim 7.

16. The kit of claim 15, further comprising nucleic acids, enzymes and buffers suitable for causing amplification of STR in DNA from said species in a multiplex PCR instrument.

17. The kit of claim 15 detecting a *Cannabis sativa* L. species comprising:

i. a multiplex cocktail of claim 12;

ii. nucleic acids having an observable marker;

iii. a transcriptase; and

iv. buffers and salts suitable for causing polymerization of STR in DNA from said *Cannabis sativa* L. species in a PCR multiplex instrument.

18. The kit of claim 15, further comprising a control sample of DNA.